<u>RAW SEQUENCE LISTING</u>

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Application Serial Number: 10/684,237

Source: 1 FWO

Date Processed by STIC: 3/24/06

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RAW SEQUENCE LISTING                    DATE: 03/24/2006
PATENT APPLICATION:  US/10/684,237      TIME: 08:38:34

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     Output Set: N:\CRF4\03242006\J684237.raw
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 1 <110> APPLICANT: Huston, J.
 2        Houston, L.L.
 3        Ring, D.
 4        Oppermann, H.
 5 <120> TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING
 6 <130> FILE REFERENCE: CIBT-P01-130
 7 <140> CURRENT APPLICATION NUMBER: US/10/684,237
 8 <141> CURRENT FILING DATE: 2003-10-10
 9 <150> PRIOR APPLICATION NUMBER: US/09/558,741
10 <151> PRIOR FILING DATE: 2000-04-26
11 <150> PRIOR APPLICATION NUMBER: 07/831,967
12 <151> PRIOR FILING DATE: 1992-02-06
13 <160> NUMBER OF SEQ ID NOS: 16
14 <170> SOFTWARE: PatentIn version 3.1
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17 <211> LENGTH: 909
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
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21 <223> OTHER INFORMATION: 741F8 sFv'
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (3)..(752)
25 <223> OTHER INFORMATION:
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28          Met Ala Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
29           1               5                  10                  15
30       cct gga gag aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc      95
31       Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
32                       20                  25                  30
33       aca aac tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta     143
34       Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
35                   35                  40                  45
36       aag tgg atg ggc tgg ata aac acc aac act gga gag cca aca tat gct     191
37       Lys Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala
38               50                  55                  60
39       gaa gag ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc     239
40       Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
41           65                  70                  75
42       act gcc tat ttg cag atc aag aag ctc aaa aat gag gac acg gct aca     287
43       Thr Ala Tyr Leu Gln Ile Lys Lys Leu Lys Asn Glu Asp Thr Ala Thr
44       80              85                  90                  95
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45        tat ttc tgt gga agg caa ttt att acc tac ggc ggg ttt gct aac tgg       335
46        Tyr Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp
47                        100                 105                 110
48        ggc caa ggg act ctg gtc act gtc tct gca tcg agc tcc tcc gga tct       383
49        Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser
50                        115                 120                 125
51        tca tct agc ggt tcc agc tcg agc gat atc gtc atg acc cag tct cct       431
52        Ser Ser Ser Gly Ser Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro
53                        130                 135                 140
54        aaa ttc atg tcc acg tca gtg gga gac agg gtc agc atc tcc tgc aag       479
55        Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys
56            145                 150                 155
57        gcc agt cag gat gtg agt act gct gta gcc tgg tat caa caa aaa cca       527
58        Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro
59        160                 165                 170                 175
60        ggg caa tct cct aaa cta ctg att tac tgg aca tcc acc cgg cac act       575
61        Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr
62                        180                 185                 190
63        gga gtc cct gat cgc ttc aca ggc agt gga tct ggg aca gat tat act       623
64        Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr
65                        195                 200                 205
66        ctc acc atc agc agt gtg cag gct gaa gac ctg gca ctt cat tac tgt       671
67        Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys
68                        210                 215                 220
69        cag caa cat tat aga gtg ccg tac acg ttc gga ggg ggg acc aag ctg       719
70        Gln Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
71            225                 230                 235
72        gag ata aaa cgg gct gat ggg gga ggt gga tgt taacggggga ggtggatgtt     772
73        Glu Ile Lys Arg Ala Asp Gly Gly Gly Gly Cys
74        240                 245                 250
75        gggtctcgtt acgttgcgga tctcgaggct atctttacta actcttaccg taaagttctg     832
76        gctcaactgt ctgcacgcaa gcttttgcag gatatcatga gcgcttaaga tccgtcgacc     892
77        tgcaggcatg caagctt                                                    909
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82  <213> ORGANISM: Artificial Sequence
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84  <223> OTHER INFORMATION: 741F8 sFv'
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88        Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
89                        20                  25                  30
90        Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys
91                    35                  40                  45
92        Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala Glu
93                50                  55                  60
94        Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr
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 95         65                   70                   75                   80
 96    Ala Tyr Leu Gln Ile Lys Lys Leu Lys Asn Glu Asp Thr Ala Thr Tyr
 97                        85                   90                   95
 98    Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp Gly
 99                   100                  105                  110
100     Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser Ser
101                  115                  120                  125
102     Ser Ser Gly Ser Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro Lys
103          130                  135                  140
104     Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys Ala
105     145                  150                  155                  160
106     Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly
107                   165                  170                  175
108     Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly
109                   180                  185                  190
110     Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu
111                   195                  200                  205
112     Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys Gln
113          210                  215                  220
114     Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
115     225                  230                  235                  240
116     Ile Lys Arg Ala Asp Gly Gly Gly Gly Cys
117                   245                  250

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120 <211> LENGTH: 779
121 <212> TYPE: DNA
122 <213> ORGANISM: Artificial Sequence
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124 <223> OTHER INFORMATION: 26-10 sFv'
125 <220> FEATURE:
126 <221> NAME/KEY: CDS
127 <222> LOCATION: (3)..(758)
128 <223> OTHER INFORMATION:
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130     cc atg gaa gtt caa ctg caa cag tct ggt cct gaa ttg gtt aaa cct      47
131        Met Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro
132         1               5                  10                  15
133     ggc gcc tct gtg cgc atg tcc tgc aaa tcc tct ggg tac att ttc acc      95
134     Gly Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr
135                        20                   25                  30
136     gac ttc tac atg aat tgg gtt cgc cag tct cat ggt aag tct cta gac     143
137     Asp Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp
138                   35                   40                   45
139     tac atc ggg tac att tcc cca tac tct ggg gtt acc ggc tac aac cag     191
140     Tyr Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln
141          50                   55                   60
142     aag ttt aaa ggt aag gcg acc ctt act gtc gac aaa tct tcc tca act     239
143     Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr
144          65                   70                   75
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145    gct tac atg gag ctg cgt tct ttg acc tct gag gac tcc gcg gta tac    287
146    Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
147    80              85              90              95
148    tat tgc gcg ggc tcc tct ggt aac aaa tgg gcc atg gat tat tgg ggt    335
149    Tyr Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly
150              100             105             110
151    cat ggt gct agc gtt act gtg agc tcc tcc gga tct tca tct agc ggt    383
152    His Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Ser Gly
153              115             120             125
154    tcc agc tcg agt gga tcc gac gtc gta atg acc cag act ccg ctg tct    431
155    Ser Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser
156              130             135             140
157    ctg ccg gtt tct ctg ggt gac cag gct tct att tct tgc cgc tct tcc    479
158    Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser
159              145             150             155
160    cag tct ctg gtc cat tct aat ggt aac act tac ctg aac tgg tac ctg    527
161    Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu
162    160             165             170             175
163    caa aag gct ggt cag tct ccg aag ctt ctg atc tac aaa gtc tct aac    575
164    Gln Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn
165              180             185             190
166    cgc ttc tct ggt gtc ccg gat cgt ttc tct ggt tct ggt tct ggt act    623
167    Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
168              195             200             205
169    gac ttc acc ctg aag atc tct cgt gtc cag gcc gaa gac ctg ggt atc    671
170    Asp Phe Thr Leu Lys Ile Ser Arg Val Gln Ala Glu Asp Leu Gly Ile
171              210             215             220
172    tac ttc tgc tct cag act act cat gta ccg ccg act ttt ggt ggt ggc    719
173    Tyr Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly
174              225             230             235
175    acc aag ctc gag att aaa cgt tcc ggg gga ggt gga tgt taactgcagc    768
176    Thr Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys
177    240             245             250
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181 <211> LENGTH: 252
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183 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: 26-10 sFv'
186 <400> SEQUENCE: 4
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189    Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr Asp
190              20              25              30
191    Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp Tyr
192              35              40              45
193    Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln Lys
194        50              55              60
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195      Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala
196      65                  70                  75                  80
197      Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
198                      85                  90                  95
199      Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly His
200                      100                 105                 110
201      Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser
202                      115                 120                 125
203      Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu
204              130                 135                 140
205      Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
206      145                 150                 155                 160
207      Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln
208                      165                 170                 175
209      Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
210                      180                 185                 190
211      Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
212                      195                 200                 205
213      Phe Thr Leu Lys Ile Ser Arg Val Gln Ala Glu Asp Leu Gly Ile Tyr
214              210                 215                 220
215      Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr
216      225                 230                 235                 240
217      Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys
218                      245                 250
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222 <212> TYPE: DNA
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225 <223> OTHER INFORMATION: 520C9 sFv
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227 <221> NAME/KEY: CDS
228 <222> LOCATION: (1)..(729)
229 <223> OTHER INFORMATION:
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232      Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
233      1               5                   10                  15
234      aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc gca aac tat      96
235      Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn Tyr
236                      20                  25                  30
237      gga atg aac tgg atg aag cag gct cca gga aag ggt tta aag tgg atg     144
238      Gly Met Asn Trp Met Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
239                      35                  40                  45
240      ggc tgg ata aac acc tac act gga cag tca aca tat gct gat gac ttc     192
241      Gly Trp Ile Asn Thr Tyr Thr Gly Gln Ser Thr Tyr Ala Asp Asp Phe
242          50                  55                  60
243      aag gaa cgg ttt gcc ttc tct ttg gaa acc tct gcc acc act gcc cat     240
244      Lys Glu Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Thr Thr Ala His
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W--> (row 230)

VERIFICATION SUMMARY   DATE: 03/24/2006
PATENT APPLICATION: **US/10/684,237**   TIME: 08:38:35

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Output Set: **N:\CRF4\03242006\J684237.raw**

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